Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Withdrawn) A Complex, comprising:

a. a first nucleic acid comprising, from 3' to 5': a Substrate Hybridization Domain and a Signal Template Domain, wherein:

i. the Substrate Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides; and

ii. the Signal Template Domain comprises a sequence of about 5 to about 100 nucleotides;

and:

b. a second nucleic acid comprising from 3' to 5': a Signal Domain, a Template Hybridization Domain and a Target Binding Domain, wherein:

i. the Signal Domain comprises a sequence of about 5 to about 100 nucleotides, which sequence shows complementarity toward and is hybridizable to the Signal Template Domain of the first nucleic acid, and of which at least two nucleotides are detectably labeled;

ii. the Template Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first nucleic acid;

iii. the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the Template Hybridization Domain.

2. (Withdrawn) The Complex of claim 1, wherein the nucleotides which comprise the first or second nucleic acid are deoxyribonucleotides.

3. (Withdrawn) The Complex of claim 1, wherein the nucleotides which comprise the Signal Domain of the second nucleic acid are deoxyribonucleotides and the nucleotides which comprise the Template Hybridization Domain and the Target Binding Domain of the second nucleic acid are ribonucleotides.

4. (Withdrawn) The Complex of claim 1, wherein the Substrate Hybridization Domain is at the 3' end of the first nucleic acid.

5. (Withdrawn) The Complex of claim 1, wherein the Substrate Hybridization Domain comprises a sequence of about 5 to about 10 nucleotides.

6. (Withdrawn) The Complex of claim 1, wherein the Substrate Hybridization Domain cannot he extended by a 5'→3' DNA polymerase.

7. (Withdrawn) The Complex of claim 6, wherein the Substrate Hybridization Domain further comprises an extension of nucleotides at the 3' end of said Substrate Hybridization 10 Domain, the extension having no complementarity to the Template Hybridization Domain of the second nucleic acid.

8. (Withdrawn) The Complex of claim 6, wherein the Substrate Hybridization Domain comprises a 3'-terminal modified nucleotide.

9. (Withdrawn) The Complex of claim 8, wherein the modification is selected from the group consisting of: a 3'-amino-modifier, a 2', 3'-dideoxynucleotide, a 3-phosphate, and a modified 3' phosphate group.

10. (Withdrawn) The Complex of claim 1, wherein the Substrate Hybridization Domain comprises at least one nucleotide which comprises a modified cytidine, which nucleotide is selected from the group consisting of: C5-methyl-dC and C5-propynyl-dC.

11. (Withdrawn) The Complex of claim 1, wherein the Signal Domain comprises a sequence of about 10 to about 50 nucleotides.

12. (Withdrawn) The Complex of claim 1, wherein the Signal Domain is at least 50%, at least 70%, at least 90% or 100% homopolymeric.

13. (Withdrawn) The Complex of claim 1, wherein at least 60%, at least 80% or 100% of the nucleotides of the Template Hybridization Domain comprise guanosine or cytidine or a combination thereof

14. (Withdrawn) The Complex of claim 1, wherein at least 60% of the nucleotides of the Template Hybridization Domain comprise guanosine or cytidine or a combination thereof, and the Signal Domain is at least 50% homopolymeric.

15. (Withdrawn) A reaction mixture for use in a process for the labeling of a nucleic acid molecule comprising:

a. a first nucleic acid comprising, from 3' to 5': a Substrate Hybridization Domain and a Signal Template Domain, wherein:

i. the Substrate Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides; and

ii. the Signal Template Domain comprises a sequence of about 5 to about 100 nucleotides;

and:

b. a second nucleic acid comprising from 3' to 5':a Template Hybridization Domain and a Target Binding Domain, wherein:

i. the Template Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first nucleic acid;

ii. the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the

Template Hybridization Domain.

16. (Withdrawn) The reaction mixture of claim 15, wherein the nucleotides which comprise the first or second nucleic acid are deoxyribonucleotides.

17. (Withdrawn) The reaction mixture of claim 15, wherein the nucleotides which comprise the first or second nucleic acid are ribonucleotides.

18. (Withdrawn) The reaction mixture of claim 15, wherein the Substrate Hybridization Domain is at the 3 end of the first nucleic acid.

19. (Withdrawn) The reaction mixture of claim 15, wherein the Substrate Hybridization Domain comprises a sequence of about 5 to about 10 nucleotides.

20. (Withdrawn) The reaction mixture of claim 15, wherein the Substrate Hybridization Domain cannot be extended by a 5'→3' DNA polymerase.

21. (Withdrawn) The reaction mixture of claim 20, wherein the Substrate Hybridization Domain further comprises an extension of nucleotides at the 3' end of said Substrate Hybridization Domain, the extension having no complementarity to the Template Hybridization Domain of the second nucleic acid.

22. (Withdrawn) The reaction mixture of claim 20, wherein the Substrate Hybridization Domain comprises a 3-terminal modified nucleotide.

23. (Withdrawn) The reaction mixture of claim 22, wherein the modification is selected from the group consisting of: a 3'-amino-modifier, a 2', 3'-dideoxynucleotide, a 3'-phosphate, and 10 a modified 3'-phosphate group.

24. (Withdrawn) The reaction mixture of claim 15, wherein the Substrate Hybridization Domain comprises at least one nucleotide which comprises a modified cytidine, which nucleotide is selected from the group consisting of: C5-methyl-dC and C5-propynyl-dC.

25. (Withdrawn) The reaction mixture of claim 15, wherein the Signal Template Domain comprises a sequence of about 10 to about 50 nucleotides.

26. (Withdrawn) The reaction mixture of claim 15, wherein the Signal Domain is at least 50%, 20 at least 70%, at least 90% or 100% homopolymeric.

27. (Withdrawn) The reaction mixture of claim 15, wherein at least 60%, at least 80% or 100% of the nucleotides of the Template Hybridization Domain comprise guanosine or cytidine or a combination thereof.

28. (Withdrawn) The reaction mixture of claim 15, wherein at least 60% of the nucleotides of the Template Hybridization Domain comprise guanosine or cytidine or a combination thereof, and the Signal Domain is at least 50% homopolymeric.

29. (Currently Amended) A method of labeling an oligonucleotide ~~a nucleic acid molecule~~, comprising the steps of:

a. hybridizing a first oligonucleotide ~~nucleic acid~~ to a second oligonucleotide ~~nucleic acid~~, wherein the first oligonucleotide ~~nucleic acid~~ comprises, from 3' to 5': a Substrate Hybridization Domain adjoining ~~and~~ a Signal Template Domain, wherein:

i. the Substrate Hybridization Domain consists of a sequence of about 5 to about ~~less than~~ 10 nucleotides; and

ii. the Signal Template Domain consists of ~~comprises~~ a sequence of about 5 to about 100 nucleotides;

and the second oligonucleotide ~~nucleic acid~~ comprises, from 3' to 5': a Template Hybridization Domain adjoining ~~and~~ a Target Binding Domain, wherein:

i. the Template Hybridization Domain consists of a sequence of about 5 to about ~~less than~~ 10 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first oligonucleotide ~~nucleic acid~~;

ii. the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the Template Hybridization Domain;

and:

b. extending the second oligonucleotide ~~nucleic acid~~ with a DNA polymerase in the presence of a labeled nucleotides to create an oligonucleotide having from 5' to 3' an unlabeled Target Binding Domain adjoining~~[[,]]~~ a Template Hybridization Domain adjoining~~[[, and]]~~ a labeled Signal Domain~~, having a complimentary sequence which shows complementarity toward and is hybridizable to the Signal Template Domain.~~

30. (Currently amended) The method of claim 29, wherein the nucleotides which comprise the first or second oligonucleotide ~~nucleic acid~~ are deoxyribonucleotides.

31. (Currently amended) The method of claim 29, wherein the ~~nucleotides which comprise the~~ first or second oligonucleotide comprise ~~nucleic acid~~ ribonucleotides.

32. (Currently amended) The method of claim 29, wherein the second oligonucleotide ~~nucleic acid~~ consists of about 15 to about 150 nucleotides.

33. (Currently amended) The method of claim 29, wherein the Substrate Hybridization Domain is at the 3' end of the first oligonucleotide ~~nucleic acid~~.

34. (Canceled)

35. (Original) The method of claim 29, wherein the Substrate Hybridization Domain cannot be extended by a 5'→3' DNA polymerase.

36. (Currently amended) The method of claim 35, wherein the Substrate Hybridization Domain further comprises an extension of nucleotides at the 3' end of said Substrate Hybridization Domain, the extension having no complementarity to the Template Hybridization Domain of the second oligonucleotide ~~nucleic acid~~.

37. (Original) The method of claim 35, wherein the Substrate Hybridization Domain comprises a 3'-terminal modified nucleotide.

38. (Original) The method of claim 37, wherein the modification is selected from the group consisting of: a 3'-amino-modifier, a 2', 3'-dideoxynucleotide, a 3'-phosphate, and a modified 3'-phosphate group.

39. (Original) The method of claim 29, wherein the Substrate Hybridization Domain comprises at least one nucleotide which comprises a modified cytidine, which nucleotide is selected from the group consisting of: C5-methyl-dC and C5-propynyl-dC.

40. (Original) The method of claim 29, wherein the Signal Template Domain comprises a sequence of about 10 to about 50 nucleotides.

41. (Original) The method of claim 29, wherein the Signal Domain is at least 50%, at least 70%, at least 90% or 100% homopolymeric.

42. (Canceled)

43. (Original) The method of claim 29, wherein at least 60% of the nucleotides of the Template Hybridization Domain comprise guanosine or cytidine or a combination thereof, and the Signal Domain is at least 50% hompolymeric.

44. (Original) The method of claim 29, wherein the extending step is carried out by a DNA polymerase selected from the group consisting of: *E. coli* DNA polymerase I holoenzyme, Klenow fragment of *E. coli* DNA polymerase I, T4 DNA polymerase, T7 DNA polymerase, and a DNA polymerase encoded by a thermophilic bacterium.

45. (Original) The method of claim 29, wherein the Template Hybridization Domain or the Substrate Hybridization Domain comprises at least one modified nucleotide, which modified nucleotide increases the hybridization affinity of said Template Hybridization Domain to said Substrate Hybridization Domain.

46. (Original) The method of claim 45, wherein at least one modified nucleotide is found in the Template Hybridization Domain.

47. (Original) The method of claim 46, wherein at least one modified nucleotide is selected from the group consisting of: C5-methyl-dC, C5-propynyl-dC, C5-propynyl-dU, and 2,6-diaminopurine.

48. (Original) The method of claim 29, wherein at least one nucleotide comprises a label selected from the group consisting of: ^{32}P, ^{33}P, ^{35}S, fluorescein, digoxigenin, biotin, Cy5, Cy3, and rhodamine.

Claims 49-54 (Canceled).

55. (Previously presented) The method of claim 29, wherein the Probe has a specific activity of at least 7 x 10^7 CPM per picomole, and wherein the Probe comprises the Target Binding Domain, the Template Hybridization Domain and the Signal Domain.

56. (Previously presented) The method of claim 29, wherein the Probe has a specific activity of at least 9 x 10^7 CPM per picomole, and wherein the Probe comprises the Target Binding Domain, the Template Hybridization Domain and the Signal Domain.

57. (Currently amended) The method of claim 29, wherein the first oligonucleotide ~~nucleic acid~~ has a hairpin loop disposed to the 5'side of the Signal Template Domain.